RAW SEQUENCE LISTING
ERROR REPORT

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Application Serial Number: *10/803,580 A*

Source: *I two*

Date Processed by STIC: *6/17/04*

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Revised 05/17/04

RAW SEQUENCE LISTING   DATE: 06/17/2004
PATENT APPLICATION: **US/10/803,580A**   TIME: 07:29:17

Input Set : **A:\SYR-HDAC-5005-C2 replacement 01.ST25.txt**
Output Set: **N:\CRF4\06172004\J803580A.raw**

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 3 <110> APPLICANT: Syrrx, Inc.
 5 <120> TITLE OF INVENTION: HISTONE DEACETYLASE INHIBITORS
 7 <130> FILE REFERENCE: SYR-HDAC-5005-C2
 9 <140> CURRENT APPLICATION NUMBER: US 10/803,580A
10 <141> CURRENT FILING DATE: 2004-03-17
12 <150> PRIOR APPLICATION NUMBER: US 60/455,437
13 <151> PRIOR FILING DATE: 2003-03-17
15 <150> PRIOR APPLICATION NUMBER: US 60/531,203
16 <151> PRIOR FILING DATE: 2003-12-19
18 <160> NUMBER OF SEQ ID NOS: 8
20 <170> SOFTWARE: PatentIn version 3.2
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 513
24 <212> TYPE: PRT
25 <213> ORGANISM: Artificial
27 <220> FEATURE:
28 <223> OTHER INFORMATION: Residues 1-482 of HDAC1 and a 6-histidine tag at the N-
terminus
30 <400> SEQUENCE: 1
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33 1               5                   10                  15
36 Thr Glu Asn Leu Tyr Phe Gln Gly Ala Met Glu Pro Gly Gly Ser Met
37             20                  25                  30
40 Ala Gln Thr Gln Gly Thr Arg Arg Lys Val Cys Tyr Tyr Tyr Asp Gly
41         35                  40                  45
44 Asp Val Gly Asn Tyr Tyr Tyr Gly Gln Gly His Pro Met Lys Pro His
45      50                  55                  60
48 Arg Ile Arg Met Thr His Asn Leu Leu Leu Asn Tyr Gly Leu Tyr Arg
49 65                  70                  75                  80
52 Lys Met Glu Ile Tyr Arg Pro His Lys Ala Asn Ala Glu Glu Met Thr
53                  85                  90                  95
56 Lys Tyr His Ser Asp Asp Tyr Ile Lys Phe Leu Arg Ser Ile Arg Pro
57              100                 105                 110
60 Asp Asn Met Ser Glu Tyr Ser Lys Gln Met Gln Arg Phe Asn Val Gly
61          115                 120                 125
64 Glu Asp Cys Pro Val Phe Asp Gly Leu Phe Glu Phe Cys Gln Leu Ser
65      130                 135                 140
68 Thr Gly Gly Ser Val Ala Ser Ala Val Lys Leu Asn Lys Gln Gln Thr
69 145                 150                 155                 160
72 Asp Ile Ala Val Asn Trp Ala Gly Gly Leu His His Ala Lys Lys Ser
73                  165                 170                 175
76 Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp Ile Val Leu Ala Ile Leu
77              180                 185                 190
80 Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr Ile Asp Ile Asp Ile
```

```
81          195                    200                    205
84 His His Gly Asp Gly Val Glu Glu Ala Phe Tyr Thr Thr Asp Arg Val
85      210                    215                    220
88 Met Thr Val Ser Phe His Lys Tyr Gly Glu Tyr Phe Pro Gly Thr Gly
89 225                    230                    235                    240
92 Asp Leu Arg Asp Ile Gly Ala Gly Lys Gly Lys Tyr Tyr Ala Val Asn
93                    245                    250                    255
96 Tyr Pro Leu Arg Asp Gly Ile Asp Asp Glu Ser Tyr Glu Ala Ile Phe
97                260                    265                    270
100 Lys Pro Val Met Ser Lys Val Met Glu Met Phe Gln Pro Ser Ala Val
101          275                    280                    285
104 Val Leu Gln Cys Gly Ser Asp Ser Leu Ser Gly Asp Arg Leu Gly Cys
105      290                    295                    300
108 Phe Asn Leu Thr Ile Lys Gly His Ala Lys Cys Val Glu Phe Val Lys
109 305                    310                    315                    320
112 Ser Phe Asn Leu Pro Met Leu Met Leu Gly Gly Gly Gly Tyr Thr Ile
113                325                    330                    335
116 Arg Asn Val Ala Arg Cys Trp Thr Tyr Glu Thr Ala Val Ala Leu Asp
117                340                    345                    350
120 Thr Glu Ile Pro Asn Glu Leu Pro Tyr Asn Asp Tyr Phe Glu Tyr Phe
121          355                    360                    365
124 Gly Pro Asp Phe Lys Leu His Ile Ser Pro Ser Asn Met Thr Asn Gln
125      370                    375                    380
128 Asn Thr Asn Glu Tyr Leu Glu Lys Ile Lys Gln Arg Leu Phe Glu Asn
129 385                    390                    395                    400
132 Leu Arg Met Leu Pro His Ala Pro Gly Val Gln Met Gln Ala Ile Pro
133                405                    410                    415
136 Glu Asp Ala Ile Pro Glu Glu Ser Gly Asp Glu Asp Glu Asp Asp Pro
137          420                    425                    430
140 Asp Lys Arg Ile Ser Ile Cys Ser Ser Asp Lys Arg Ile Ala Cys Glu
141          435                    440                    445
144 Glu Glu Phe Ser Asp Ser Glu Glu Glu Gly Glu Gly Gly Arg Lys Asn
145      450                    455                    460
148 Ser Ser Asn Phe Lys Lys Ala Lys Arg Val Lys Thr Glu Asp Glu Lys
149 465                    470                    475                    480
152 Glu Lys Asp Pro Glu Glu Lys Lys Glu Val Thr Glu Glu Glu Lys Thr
153          485                    490                    495
156 Lys Glu Glu Lys Pro Glu Ala Lys Gly Val Lys Glu Glu Val Lys Leu
157          500                    505                    510
160 Ala
164 <210> SEQ ID NO: 2
165 <211> LENGTH: 1542
166 <212> TYPE: DNA
167 <213> ORGANISM: Artificial
169 <220> FEATURE:
170 <223> OTHER INFORMATION: DNA sequence encoding residues 1-482 of HDAC1 and a 6-
histidine
171          tag at the N-terminus
173 <400> SEQUENCE: 2
174 atgtcgtact accatcacca tcaccatcac gattacgata tcccaacgac cgaaaacctg        60
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[Handwritten annotation]: please explain the remaining residues, per the total length of the sequence

Input Set : **A:\SYR-HDAC-5005-C2 replacement 01.ST25.txt**
Output Set: **N:\CRF4\06172004\J803580A.raw**

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176 tattttcagg gcgccatgga acccggggga tccatggcgc agacgcaggg cacccggagg   120
178 aaagtctgtt actactacga cggggatgtt ggaaattact attatggaca aggccaccca   180
180 atgaagcctc accgaatccg catgactcat aatttgctgc tcaactatgg tctctaccga   240
182 aaaatggaaa tctatcgccc tcacaaagcc aatgctgagg agatgaccaa gtaccacagc   300
184 gatgactaca ttaaattctt gcgctccatc cgtccagata acatgtcgga gtacagcaag   360
186 cagatgcaga gattcaacgt tggtgaggac tgtccagtat tcgatggcct gtttgagttc   420
188 tgtcagttgt ctactggtgg ttctgtggca agtgctgtga aacttaataa gcagcagacg   480
190 gacatcgctg tgaattgggc tgggggcctg caccatgcaa agaagtccga ggcatctggc   540
192 ttctgttacg tcaatgatat cgtcttggcc atcctggaac tgctaaagta tcaccagagg   600
194 gtgctgtaca ttgacattga tattcaccat ggtgacggcg tggaagaggc cttctacacc   660
196 acggaccggg tcatgactgt gtcctttcat aagtatggag agtacttccc aggaactggg   720
198 gacctacggg atatcggggc tggcaaaggc aagtattatg ctgttaacta cccgctccga   780
200 gacgggattg atgacgagtc ctatgaggcc attttcaagc cggtcatgtc caaagtaatg   840
202 gagatgttcc agcctagtgc ggtggtctta cagtgtggct cagactccct atctggggat   900
204 cggttaggtt gcttcaatct aactatcaaa ggacacgcca agtgtgtgga atttgtcaag   960
206 agctttaacc tgcctatgct gatgctggga ggcggtggtt acaccattcg taacgttgcc  1020
208 cggtgctgga catatgagac agctgtggcc ctggatacgg agatccctaa tgagcttcca  1080
210 tacaatgact actttgaata ctttggacca gatttcaagc tccacatcag tccttccaat  1140
212 atgactaacc agaacacgaa tgagtacctg gagaagatca aacagcgact gtttgagaac  1200
214 cttagaatgc tgccgcacgc acctggggtc caaatgcagg cgattcctga ggacgccatc  1260
216 cctgaggaga gtggcgatga ggacgaagac gaccctgaca gcgcatctc gatctgctcc  1320
218 tctgacaaac gaattgcctg tgaggaagag ttctccgatt ctgaagagga gggagagggg  1380
220 ggccgcaaga actcttccaa cttcaaaaaa gccaagagag tcaaaacaga ggatgaaaaa  1440
222 gagaaagacc cagaggagaa gaaagaagtc accgaagagg agaaaaccaa ggaggagaag  1500
224 ccagaagcca aagggggtcaa ggaggaggtc aagttggcct ga                      1542
227 <210> SEQ ID NO: 3
228 <211> LENGTH: 498
229 <212> TYPE: PRT
230 <213> ORGANISM: Artificial
232 <220> FEATURE:
233 <223> OTHER INFORMATION: Residues 1-488 of HDAC2 and a 6-histidine tag at the C-
terminus
235 <400> SEQUENCE: 3
237 Met Gly Ser Met Ala Tyr Ser Gln Gly Gly Gly Lys Lys Lys Val Cys
238 1               5                   10                  15
241 Tyr Tyr Tyr Asp Gly Asp Ile Gly Asn Tyr Tyr Tyr Gly Gln Gly His
242                 20                  25                  30
245 Pro Met Lys Pro His Arg Ile Arg Met Thr His Asn Leu Leu Leu Asn
246             35                  40                  45
249 Tyr Gly Leu Tyr Arg Lys Met Glu Ile Tyr Arg Pro His Lys Ala Thr
250         50                  55                  60
253 Ala Glu Glu Met Thr Lys Tyr His Ser Asp Glu Tyr Ile Lys Phe Leu
254 65                  70                  75                  80
257 Arg Ser Ile Arg Pro Asp Asn Met Ser Glu Tyr Ser Lys Gln Met Gln
258                 85                  90                  95
261 Arg Phe Asn Val Gly Glu Asp Cys Pro Val Phe Asp Gly Leu Phe Glu
262                 100                 105                 110
265 Phe Cys Gln Leu Ser Thr Gly Gly Ser Val Ala Gly Ala Val Lys Leu
266             115                 120                 125
269 Asn Arg Gln Gln Thr Asp Met Ala Val Asn Trp Ala Gly Gly Leu His
```

```
270      130                   135                   140
273 His Ala Lys Lys Ser Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp Ile
274 145                   150                   155                   160
277 Val Leu Ala Ile Leu Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr
278                   165                   170                   175
281 Ile Asp Ile Asp Ile His His Gly Asp Gly Val Glu Glu Ala Phe Tyr
282                   180                   185                   190
285 Thr Thr Asp Arg Val Met Thr Val Ser Phe His Lys Tyr Gly Glu Tyr
286             195                   200                   205
289 Phe Pro Gly Thr Gly Asp Leu Arg Asp Ile Gly Ala Gly Lys Gly Lys
290       210                   215                   220
293 Tyr Tyr Ala Val Asn Phe Pro Met Arg Asp Gly Ile Asp Asp Glu Ser
294 225                   230                   235                   240
297 Tyr Gly Gln Ile Phe Lys Pro Ile Ile Ser Lys Val Met Glu Met Tyr
298                   245                   250                   255
301 Gln Pro Ser Ala Val Val Leu Gln Cys Gly Ala Asp Ser Leu Ser Gly
302             260                   265                   270
305 Asp Arg Leu Gly Cys Phe Asn Leu Thr Val Lys Gly His Ala Lys Cys
306             275                   280                   285
309 Val Glu Val Val Lys Thr Phe Asn Leu Pro Leu Leu Met Leu Gly Gly
310       290                   295                   300
313 Gly Gly Tyr Thr Ile Arg Asn Val Ala Arg Cys Trp Thr Tyr Glu Thr
314 305                   310                   315                   320
317 Ala Val Ala Leu Asp Cys Glu Ile Pro Asn Glu Leu Pro Tyr Asn Asp
318             325                   330                   335
321 Tyr Phe Glu Tyr Phe Gly Pro Asp Phe Lys Leu His Ile Ser Pro Ser
322             340                   345                   350
325 Asn Met Thr Asn Gln Asn Thr Pro Glu Tyr Met Glu Lys Ile Lys Gln
326             355                   360                   365
329 Arg Leu Phe Glu Asn Leu Arg Met Leu Pro His Ala Pro Gly Val Gln
330       370                   375                   380
333 Met Gln Ala Ile Pro Glu Asp Ala Val His Glu Asp Ser Gly Asp Glu
334 385                   390                   395                   400
337 Asp Gly Glu Asp Pro Asp Lys Arg Ile Ser Ile Arg Ala Ser Asp Lys
338             405                   410                   415
341 Arg Ile Ala Cys Asp Glu Glu Phe Ser Asp Ser Glu Asp Glu Gly Glu
342             420                   425                   430
345 Gly Gly Arg Arg Asn Val Ala Asp His Lys Lys Gly Ala Lys Lys Ala
346             435                   440                   445
349 Arg Ile Glu Glu Asp Lys Lys Glu Thr Glu Asp Lys Lys Thr Asp Val
350       450                   455                   460
353 Lys Glu Glu Asp Lys Ser Lys Asp Asn Ser Gly Glu Lys Thr Asp Thr
354 465                   470                   475                   480
357 Lys Gly Thr Lys Ser Glu Gln Leu Ser Asn Pro Gly His His His His
358             485                   490                   495
361 His His
365 <210> SEQ ID NO: 4
366 <211> LENGTH: 1497
367 <212> TYPE: DNA
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SAME error

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368 <213> ORGANISM: Artificial
370 <220> FEATURE:
371 <223> OTHER INFORMATION: DNA sequence encoding residues 1-488 of HDAC2 and a 6-
histidine
372           tag at the C-terminus
374 <400> SEQUENCE: 4
375 atgggatcca tggcgtacag tcaaggaggc ggcaaaaaaa aagtctgcta ctactacgac      60
377 ggtgatattg gaaattatta ttatggacag ggtcatccca tgaagcctca tagaatccgc     120
379 atgacccata acttgctgtt aaattatggc ttatacagaa aaatggaaat atataggccc     180
381 cataaagcca ctgccgaaga aatgacaaaa tatcacagtg atgagtatat caaatttcta     240
383 cggtcaataa gaccagataa catgtctgag tatagtaagc agatgcagag atttaatgtt     300
385 ggagaagatt gtccagtgtt tgatggactc tttgagtttt gtcagctctc aactggcggt     360
387 tcagttgctg gagctgtgaa gttaaaccga caacagactg atatggctgt taattgggct     420
389 ggaggattac atcatgctaa gaaatcagaa gcatcaggat tctgttacgt taatgatatt     480
391 gtgcttgcca tccttgaatt actaaagtat catcagagag tcttatatat tgatatagat     540
393 attcatcatg gtgatggtgt tgaagaagct ttttatacaa cagatcgtgt aatgacggta     600
395 tcattccata aatatgggga atactttcct ggcacaggag acttgaggga tattggtgct     660
397 ggaaaaggca aatactatgc tgtcaatttt ccaatgagag atggtataga tgatgagtca     720
399 tatgggcaga tatttaagcc tattatctca aaggtgatgg agatgtatca acctagtgct     780
401 gtggtattac agtgtggtgc agactcatta tctggtgata gactggggttg tttcaatcta     840
403 acagtcaaag gtcatgctaa atgtgtagaa gttgtaaaaa cttttaactt accattactg     900
405 atgcttggag gaggtggcta cacaatccgt aatgttgctc gatgttggac atatgagact     960
407 gcagttgccc ttgattgtga gattcccaat gagttgccat ataatgatta ctttgagtat    1020
409 tttggaccag acttcaaact gcatattagt ccttcaaaca tgacaaacca gaacactcca    1080
411 gaatatatgg aaaagataaa acagcgtttg tttgaaaatt tgcgcatgtt acctcatgca    1140
413 cctggtgtcc agatgcaagc tattccagaa gatgctgttc atgaagacag tggagatgaa    1200
415 gatggagaag atccagacaa gagaatttct attcgagcat cagacaagcg gatagcttgt    1260
417 gatgaagaat tctcagattc tgaggatgaa ggagaaggag gtcgaagaaa tgtggctgat    1320
419 cataagaaag gagcaaagaa agctagaatt gaagaagata agaaagaaac agaggacaaa    1380
421 aaaacagacg ttaaggaaga agataaatcc aaggacaaca gtggtgaaaa aacagatacc    1440
423 aaaggaacca aatcagaaca gctcagcaac cccgggcatc accatcacca tcactaa      1497
426 <210> SEQ ID NO: 5
427 <211> LENGTH: 782
428 <212> TYPE: PRT
429 <213> ORGANISM: Artificial
431 <220> FEATURE:
432 <223> OTHER INFORMATION: Residues 73-845 of HDAC6 and a 6-histidine tag at the C-
terminus
434 <400> SEQUENCE: 5
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437 1               5                   10                  15
440 Gly Leu Val Leu Asp Glu Gln Leu Asn Glu Phe His Cys Leu Trp Asp
441             20                  25                  30
444 Asp Ser Phe Pro Glu Gly Pro Glu Arg Leu His Ala Ile Lys Glu Gln
445         35                  40                  45
448 Leu Ile Gln Glu Gly Leu Leu Asp Arg Cys Val Ser Phe Gln Ala Arg
449     50                  55                  60
452 Phe Ala Glu Lys Glu Glu Leu Met Leu Val His Ser Leu Glu Tyr Ile
453 65                  70                  75                  80
456 Asp Leu Met Glu Thr Thr Gln Tyr Met Asn Glu Gly Glu Leu Arg Val
457                 85                  90                  95
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SAME error

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 06/17/2004
PATENT APPLICATION: **US/10/803,580A**   TIME: 07:29:18

Input Set : **A:\SYR-HDAC-5005-C2 replacement 01.ST25.txt**
Output Set: **N:\CRF4\06172004\J803580A.raw**

Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4,5,6,7,8

VERIFICATION SUMMARY   DATE: 06/17/2004
PATENT APPLICATION: **US/10/803,580A**   TIME: 07:29:18

Input Set : **A:\SYR-HDAC-5005-C2 replacement 01.ST25.txt**
Output Set: **N:\CRF4\06172004\J803580A.raw**